

### **Amendments to the Claims:**

*This listing of claims will replace all prior versions, and listings, of claims in the application:*

1. (currently amended) A method for predicting nucleic acid hybridization thermodynamics in a solution, the method comprising:

providing a database of thermodynamics parameters;

receiving hybridization information which represents at least one target sequence and at least one of a primer and a probe, wherein a length of the target sequence is longer than a length of the at least one of a primer and a probe;

receiving correction data;

receiving a first set of data which represents hybridization conditions;

calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data, wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes;

~~statistically weighting the hybridization thermodynamics of more than one individual single stranded and bimolecular complexes; and~~

calculating an equilibrium concentration for a species of a molecular complex in the solution at a plurality of temperatures using statistical weighing and the nucleic acid hybridization thermodynamics; and

outputting at least one the equilibrium concentration of at least one species to a user output interface.

2. (cancelled)

3. (previously presented) The method as claimed in claim 1 wherein the correction data includes folding correction data.

4. (previously presented) The method as claimed in claim 1 wherein the correction data includes linear correction data.

5. (original) The method as claimed in claim 1 wherein the thermodynamic parameters include DNA thermodynamic parameters.

6. (original) The method as claimed in claim 5 wherein the DNA thermodynamic parameters include dangling end parameters.

7. (original) The method as claimed in claim 5 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

8. (original) The method as claimed in claim 5 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

9. (original) The method as claimed in claim 1 wherein the thermodynamic parameters include RNA thermodynamic parameters.

10. (original) The method as claimed in claim 1 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

11. (original) The method as claimed in claim 1 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

12. (currently amended) The method as claimed in claim 1 wherein the hybridization information represents top and bottom strand sequences which form a duplex and wherein the nucleic acid hybridization thermodynamics are calculated for the duplex.

13. (currently amended) The method as claimed in claim 1 wherein the hybridization information represents at least a section of [[a]] the target sequence and a length of at least one primer or probe complimentary to the at least a section of the target sequence.

14. (currently amended) The method as claimed in claim 13 wherein the nucleic acid hybridization thermodynamics are calculated for a plurality of primers or probes complementary to the at least a section of the target sequence.

15. (currently amended) The method as claimed in claim 1 wherein the hybridization information represents at least a section of [[a]] the target sequence and a primer or probe.

16. (currently amended) The method as claimed in claim 15 wherein a length of the at least a section of the target sequence is longer than a length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

17. (currently amended) The method as claimed in claim 14 wherein hybridization information represents at least a section of [[a]] the target sequence and a primer or probe and wherein a length of [[a]] the at least a section of the target sequence is longer than the length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

18. (previously presented) The method as claimed in claim 1 further comprising, calculating concentration of each species in a solution at a plurality of temperatures.

19. (canceled)

20. (currently amended) The method as claimed in claim ~~19~~ 1 wherein the nucleic acid hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the method further comprises correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

21. (currently amended) A system for predicting nucleic acid hybridization thermodynamics in a solution, the system comprising:

a database of thermodynamics parameters;

means for receiving hybridization information which represents at least one target sequence;

means for receiving correction data;

means for receiving a first set of data which represents hybridization conditions;

means for calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data;

~~means for statistically weighting the hybridization thermodynamics of more than one individual single stranded and bimolecular complexes; and~~

means for calculating an equilibrium concentration for a species of a molecular complex in the solution at a plurality of temperatures using statical weighing and the nucleic acid hybridization thermodynamics; and

means for outputting ~~at least one~~ the equilibrium concentration ~~of at least one species~~ to a user output interface.

22. (cancelled)

23. (previously presented) The system as claimed in claim 21 wherein the correction data includes folding correction data.

24. (previously presented) The system as claimed in claim 21 wherein the correction data includes linear correction data.

25. (original) The system as claimed in claim 21 wherein the thermodynamic parameters include DNA thermodynamic parameters.

26. (original) The system as claimed in claim 25 wherein the DNA thermodynamic parameters include dangling end parameters.

27. (original) The system as claimed in claim 25 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

28. (original) The system as claimed in claim 25 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

29. (original) The system as claimed in claim 21 wherein the thermodynamic parameters include RNA thermodynamic parameters.

30. (original) The system as claimed in claim 21 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

31. (original) The system as claimed in claim 21 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

32. (currently amended) The system as claimed in claim 21 wherein the hybridization information represents top and bottom strand sequences which form a duplex and wherein the nucleic acid hybridization thermodynamics are calculated for the duplex.

33. (currently amended) The system as claimed in claim 21 wherein the hybridization information represents at least a section of [[a]] the target sequence and a length of at least one primer or probe complimentary to the at least a section of the target sequence.

34. (currently amended) The system as claimed in claim 33 wherein the nucleic acid hybridization thermodynamics are calculated for a plurality of primers or probes complementary to the at least a section of the target sequence.

35. (currently amended) The system as claimed in claim 21 wherein the hybridization information represents at least a section of [[a]] the target sequence and a primer or probe.

36. (currently amended) The system as claimed in claim 35 wherein a length of the at least a section of the target sequence is longer than a length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

37. (currently amended) The system as claimed in claim 34 wherein hybridization information represents at least a section of [[a]] the target sequence and a primer or probe and wherein a length of [[a]] the at least a section of the target sequence is longer than the length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

38. (canceled)

39. (currently amended) The system as claimed in claim 38 21 wherein hybridization information also represents a primer or probe and wherein the length of the target sequence is longer than a length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex

and for competitive mismatch complexes and wherein the system further comprises means for calculating concentration of every species in ~~[[a]]~~ the solution at a plurality of temperatures.

40. (currently amended) The system as claimed in claim 39 wherein the nucleic acid hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the system further comprises means for correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

41. (currently amended) A computer-readable storage medium having stored therein a database of thermodynamics parameters and a computer program which executes the steps of:

receiving hybridization information which represents at least one target sequence in a solution;

receiving correction data;

receiving a first set of data which represents hybridization conditions;

calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data; and

~~statistically weighting the hybridization thermodynamics of more than one individual single stranded and bimolecular complexes; and~~

calculating an equilibrium concentration for a species of a molecular complex in the solution at a plurality of temperatures using statistical weighing and the nucleic acid hybridization thermodynamics; and

outputting at least one the equilibrium concentration of at least one species to a user output interface.

42. (cancelled)

43. (previously amended) The storage medium as claimed in claim 41 wherein the correction data includes folding correction data.

44. (previously amended) The storage medium as claimed in claim 41 wherein the correction data includes linear correction data.

45. (original) The storage medium as claimed in claim 41 wherein the thermodynamic parameters include DNA thermodynamic parameters.

46. (original) The storage medium as claimed in claim 45 wherein the DNA thermodynamic parameters include dangling end parameters.

47. (original) The storage medium as claimed in claim 45 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

48. (original) The storage medium as claimed in claim 41 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

49. (original) The storage medium as claimed in claim 41 wherein the thermodynamic parameters include RNA thermodynamic parameters.

50. (original) The storage medium as claimed in claim 41 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

51. (original) The storage medium as claimed in claim 41 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

52. (currently amended) The storage medium as claimed in claim 41 wherein the hybridization information represents top and bottom strand sequences which form



a duplex and wherein the nucleic acid hybridization thermodynamics are calculated for the duplex.

53. (currently amended) The storage medium as claimed in claim 41 wherein the hybridization information represents at least a section of [[a]] the target sequence and a length of at least one primer or probe complimentary to the at least a section of the target sequence.

54. (currently amended) The storage medium as claimed in claim 53 wherein the nucleic acid hybridization thermodynamics are calculated for a plurality of primers or probes complementary to the at least a section of the target sequence.

55. (currently amended) The storage medium as claimed in claim 41 wherein the hybridization information represents at least a section of [[a]] the target sequence and a primer or probe.

56. (currently amended) The storage medium as claimed in claim 55 wherein a length of the at least a section of the target sequence is longer than a length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

57. (currently amended) The storage medium as claimed in claim 54 wherein hybridization information represents at least a section of [[a]] the target sequence and a primer or probe and wherein a length of [[a]] the at least a section of the target sequence is longer than the length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

58. (canceled)

59. (currently amended) The storage medium as claimed in claim ~~58~~ 41 wherein hybridization information also represents a primer or probe and wherein the length of the target is longer than a length of the primer or probe and wherein the nucleic acid hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes and wherein the program executes the step of calculating concentration of every species in a solution at a plurality of temperatures.

60. (currently amended) The storage medium as claimed in claim 59 wherein the nucleic acid hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the program executes the step of correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

61. (new) A method for predicting nucleic acid hybridization thermodynamics, the method comprising:

providing a database of thermodynamics parameters;

receiving nucleic acid hybridization information which represents at least one sequence;

receiving correction data, wherein the correction data includes at least one of folding correction data and linear correction data;

receiving a first set of data which represents hybridization conditions;

calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data; and

outputting the nucleic acid hybridization thermodynamics to a user output interface.

62. (new) A system for predicting nucleic acid hybridization thermodynamics, the system comprising:

a database of thermodynamics parameters;

means for receiving hybridization information which represents at least one sequence;

means for receiving correction data, wherein the correction data includes at least one of folding correction data and linear correction data;

means for receiving a first set of data which represents hybridization conditions;

means for calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data; and

outputting the nucleic acid hybridization thermodynamics to a user output interface.

63. (new) A computer-readable storage medium having stored therein a database of thermodynamics parameters and a computer program which executes the steps of:

receiving hybridization information which represents at least one sequence;

receiving correction data, wherein the correction data includes at least one of folding correction data and linear correction data;

receiving a first set of data which represents hybridization conditions;

calculating nucleic acid hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data; and

outputting the nucleic acid hybridization thermodynamics to a user output interface.